

1600 #4

OIPE

2604

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/943,780

DATE: 01/07/2002

TIME: 16:29:39

Input Set : N:\Crf3\RULE60\09943780.raw

Output Set: N:\CRF3\01072602\I943780.raw

RECEIVED  
JAN 24 2002  
Technology Center 2600RECEIVED  
JAN 25 2002  
TECH CENTER 1600/2900

ENTERED

RECEIVED  
JAN 22 2002  
JC 2880 MAIL ROOM

1 <110> APPLICANT: Baker, Kevin  
 2 Botstein, David  
 3 Eaton, Dan  
 4 Ferrara, Napoleone  
 5 Filvaroff, Ellen  
 6 Gerritsen, Mary  
 7 Goddard, Audrey  
 8 Godowski, Paul  
 9 Grimaldi, Christopher  
 10 Gurney, Austin  
 11 Hillan, Kenneth  
 12 Kljavin, Ivar  
 13 Napier, Mary  
 14 Roy, Margaret  
 15 Tumas, Daniel  
 16 Wood, William  
 17 <120> TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND  
 18 ACIDS ENCODING THE SAME  
 19 <130> FILE REFERENCE: P2548P1C1  
 20 <140> CURRENT APPLICATION NUMBER: 09/943,780  
 21 <141> CURRENT FILING DATE: 2001-08-30  
 22 <150> PRIOR APPLICATION NUMBER: 09/866,028  
 23 <151> PRIOR FILING DATE: 2001-05-25  
 27 <160> NUMBER OF SEQ ID NOS: 120  
 29 <210> SEQ ID NO: 1  
 30 <211> LENGTH: 2454  
 31 <212> TYPE: DNA  
 32 <213> ORGANISM: Homo Sapien  
 33 <400> SEQUENCE: 1  
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 36 ctcactttt cttcttacac agtgtctgag aacatttaca ttatagataa 150  
 37 gtagtacatg gtggataact tctacttta ggaggactac tctcttctga 200  
 38 cagtcctaga ctggtcttct acactaagac accatgaagg agtatgtgct 250  
 39 cctattattc ctggctttgt gctctgcaa acccttctt agcccttcac 300  
 40 acatgcact gaagaatatg atgctgaagg atatggaaga cacagatgat 350  
 41 gatgatgatg atgatgatga tgatgatgat gatgaggaca actctctttt 400  
 42 tccaacaaga gagccaagaa gccattttt tccatttgat ctgtttccaa 450  
 43 tgtgtccatt tggatgtcag tgctattcac gagttgtaca ttgctcagat 500  
 44 ttaggtttga cctcagtccc aaccaacatt ccatttgata ctogaatgct 550  
 45 tgatcttcaa aacaataaaa ttaaggaaat caaagaaaat gattttaaag 600  
 46 gactcacttc actttatggt ctgacctga acaacaacaa gctaacgaag 650  
 47 attcacccaa aagcctttct aaccacaaag aagttgcgaa ggctgtatct 700  
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 51 tgataataat gggatagagc caggggcatt tgaaggggtg acggtgttcc 900

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52  atatcagaat tgcagaagca aaactgacct cagttcctaa aggcttacca 950
53  ccaactttat tggagcttca cttagattat aataaaaattt caacagtggg 1000
54  acttgaggat tttaaacgat acaaagaact acaaaggctg ggcctaggaa 1050
55  acaacaaaaat cacagatata gaaaatggga gtcttgctaa cataccacgt 1100
56  gtgagagaaa tacatttgga aaacaataaa ctaaaaaaaaaa tcccttcagg 1150
57  attaccagag ttgaaatacc tccagataat cttccttcat tctaattcaa 1200
58  ttgcaagagt gggagttaa gacttctgtc caacagtgcc aaagatgaag 1250
59  aaatctttat acagtgcaat aagtttattc aacaacccgg tgaaatactg 1300
60  ggaaatgcaa cctgcaacat ttcgttggtg tttgagcaga atgagtgttc 1350
61  agcttgggaa ctttggaaatg taataattag taattggtta tgtccattta 1400
62  atataagatt caaaaatccc tacatttgga atacttgaac tctattaata 1450
63  atggtagtat tatatataca agcaaatac tattctcaag tggtaagtcc 1500
64  actgacttat tttatgacaa gaaatttcaa cggaattttg ccaaactatt 1550
65  gatacataag gggttgagag aaacaagcat ctattgcagt ttcttttttg 1600
66  cgtacaaaatg atcttacata aatctcatgc ttgaccattc ctttcttcat 1650
67  aacaaaaaag taagatatcc ggtatttaac actttgttat caagcacatt 1700
68  ttaaaaagaa ctgtactgta aatggaatgc ttgacttagc aaaatttgtg 1750
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70  agagtgcatt acactattct tattctttag taactgggt agtactgtaa 1850
71  tatttttaat catcttaaag tatgatttga tataatctta ttgaaattac 1900
72  cttatcatgt cttagagccc gtctttatgt ttaaaactaa tttcttaaaa 1950
73  taaagccttc agtaaagtgt cattaccaac ttgataaatg ctactcataa 2000
74  gagctgggtt ggggctatag catatgcttt ttttttttta attattacct 2050
75  gatttaaaaa tctctgtaaa aacgtgtagt gtttcataaa atctgtaact 2100
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77  aggctatata acattgccac ttcaactcta aggaatatatt ttgagatata 2200
78  cctttggaag accttgcttg gaagagcctg gacactaaca attctacacc 2250
79  aaattgtctc ttcaaatacg tatggactgg ataactctga gaaacacatc 2300
80  tagtataact gaataagcag atcatcaaat taaacagaca gaaaccgaaa 2350
81  gctctatata aatgctcaga gttctttatg tattttcttat tggcattcaa 2400
82  catatgtaaa atcagaaaac agggaaattt tcattaaaaa tattggtttg 2450

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85 &lt;210&gt; SEQ ID NO: 2

86 &lt;211&gt; LENGTH: 379

87 &lt;212&gt; TYPE: PRT

88 &lt;213&gt; ORGANISM: Homo Sapien

89 &lt;400&gt; SEQUENCE: 2

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91      1              5              10              15
92  Lys Pro Phe Phe Ser Pro Ser His Ile Ala Leu Lys Asn Met Met
93      20              25              30
94  Leu Lys Asp Met Glu Asp Thr Asp Asp Asp Asp Asp Asp Asp
95      35              40              45
96  Asp Asp Asp Asp Asp Glu Asp Asn Ser Leu Phe Pro Thr Arg Glu
97      50              55              60
98  Pro Arg Ser His Phe Phe Pro Phe Asp Leu Phe Pro Met Cys Pro
99      65              70              75
100 Phe Gly Cys Gln Cys Tyr Ser Arg Val Val His Cys Ser Asp Leu
101      80              85              90

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102	Gly	Leu	Thr	Ser	Val	Pro	Thr	Asn	Ile	Pro	Phe	Asp	Thr	Arg	Met
103					95					100					105
104	Leu	Asp	Leu	Gln	Asn	Asn	Lys	Ile	Lys	Glu	Ile	Lys	Glu	Asn	Asp
105					110					115					120
106	Phe	Lys	Gly	Leu	Thr	Ser	Leu	Tyr	Gly	Leu	Ile	Leu	Asn	Asn	Asn
107					125					130					135
108	Lys	Leu	Thr	Lys	Ile	His	Pro	Lys	Ala	Phe	Leu	Thr	Thr	Lys	Lys
109					140					145					150
110	Leu	Arg	Arg	Leu	Tyr	Leu	Ser	His	Asn	Gln	Leu	Ser	Glu	Ile	Pro
111					155					160					165
112	Leu	Asn	Leu	Pro	Lys	Ser	Leu	Ala	Glu	Leu	Arg	Ile	His	Glu	Asn
113					170					175					180
114	Lys	Val	Lys	Lys	Ile	Gln	Lys	Asp	Thr	Phe	Lys	Gly	Met	Asn	Ala
115					185					190					195
116	Leu	His	Val	Leu	Glu	Met	Ser	Ala	Asn	Pro	Leu	Asp	Asn	Asn	Gly
117					200					205					210
118	Ile	Glu	Pro	Gly	Ala	Phe	Glu	Gly	Val	Thr	Val	Phe	His	Ile	Arg
119					215					220					225
120	Ile	Ala	Glu	Ala	Lys	Leu	Thr	Ser	Val	Pro	Lys	Gly	Leu	Pro	Pro
121					230					235					240
122	Thr	Leu	Leu	Glu	Leu	His	Leu	Asp	Tyr	Asn	Lys	Ile	Ser	Thr	Val
123					245					250					255
124	Glu	Leu	Glu	Asp	Phe	Lys	Arg	Tyr	Lys	Glu	Leu	Gln	Arg	Leu	Gly
125					260					265					270
126	Leu	Gly	Asn	Asn	Lys	Ile	Thr	Asp	Ile	Glu	Asn	Gly	Ser	Leu	Ala
127					275					280					285
128	Asn	Ile	Pro	Arg	Val	Arg	Glu	Ile	His	Leu	Glu	Asn	Asn	Lys	Leu
129					290					295					300
130	Lys	Lys	Ile	Pro	Ser	Gly	Leu	Pro	Glu	Leu	Lys	Tyr	Leu	Gln	Ile
131					305					310					315
132	Ile	Phe	Leu	His	Ser	Asn	Ser	Ile	Ala	Arg	Val	Gly	Val	Asn	Asp
133					320					325					330
134	Phe	Cys	Pro	Thr	Val	Pro	Lys	Met	Lys	Lys	Ser	Leu	Tyr	Ser	Ala
135					335					340					345
136	Ile	Ser	Leu	Phe	Asn	Asn	Pro	Val	Lys	Tyr	Trp	Glu	Met	Gln	Pro
137					350					355					360
138	Ala	Thr	Phe	Arg	Cys	Val	Leu	Ser	Arg	Met	Ser	Val	Gln	Leu	Gly
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147	<223>	OTHER INFORMATION:	Synthetic Oligonucleotide Probe												
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152	<211>	LENGTH:	24												

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153 <212> TYPE: DNA
154 <213> ORGANISM: Artificial Sequence
155 <220> FEATURE:
156 <223> OTHER INFORMATION: Synthetic Oligonucleotide Probe
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161 <211> LENGTH: 50
162 <212> TYPE: DNA
163 <213> ORGANISM: Artificial Sequence
164 <220> FEATURE:
165 <223> OTHER INFORMATION: Synthetic Oligonucleotide Probe
166 <400> SEQUENCE: 5
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169 <210> SEQ ID NO: 6
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171 <212> TYPE: DNA
172 <213> ORGANISM: Homo Sapien
173 <400> SEQUENCE: 6
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202      gtgctgccgg ctacgccagc ctacgctgct taggaaatgg ctccctgatc 1450
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206 ggtgcccag gggctcatat gctgctgcag aatgagctct tcctgaacgt 1650
207 gggcaccaag gaattcccag acggagagct tcgggggcac gtggctgccc 1700
208 tgccctactg tgggcatagc gcccgccatg acacgctgcc cgtgccccta 1750
209 gcaggagccc tgggtgtacc ccctgtgaag agccaagcag cagggcacgc 1800
210 ctggctttcc ttggataccc actgtcacct gcactatgaa gtgctgtctg 1850
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212 cctcctggaa cgccagggcc tcggcggtg ctgaagggat tctatggctc 1950
213 agaggcccaag ggtgtggtga aggacctgga gccggaactg ctgcggcacc 2000
214 tggcaaaaag catggcctcc ctgatgatca ccaccaagg tagccccaga 2050
215 ggggagctcc gagggcaggt gcacatagcc aaccaatgtg aggttggcgg 2100
216 actgcgcctg gaggcggccg gggccgaggg ggtgcgggcg ctgggggctc 2150
217 cggatacagc ctctgctgcg ccgcctgtgg tgcttggctc cccggcccta 2200
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240 tcttactca gcaccaaggg ccccgacac tccactcctg ctgcccctga 3350
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246 &lt;212&gt; TYPE: PRT

247 &lt;213&gt; ORGANISM: Homo Sapien

248 &lt;400&gt; SEQUENCE: 7

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251 Leu Leu Leu Leu Gly Ser Arg Pro Ala Arg Gly Ala Gly Pro Glu
252 20 25 30
253 Pro Pro Val Leu Pro Ile Arg Ser Glu Lys Glu Pro Leu Pro Val

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**VERIFICATION SUMMARY**

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